SEQUENCE LISTING

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<120> DIAGNOSTICS AND THERAPEUTICS FOR OCULAR ABNORMALITIES

<130> 020618-000120US

<140> 10/007,270
<141> 2001-11-08

<150> US 09/430,195
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            20                  25                  30

Thr Lys Asp Ile Asp Asn Pro Pro Arg Asn Glu Thr Thr Glu Ser Thr
        35                  40                  45

Glu Lys Met Tyr Lys Met Ser Thr Met Arg Arg Ile Phe Asp Leu Ala
    50                  55                  60

Lys His Arg Thr Lys Arg Ser Ala Phe Phe Pro Thr Gly Val Lys Val
65                  70                  ·75                  80

Cys Pro Gln Glu Ser Met Lys Gln Ile Leu Asp Ser Leu Gln Ala Tyr
                85                  90                  95

Tyr Arg Leu Arg Val Cys Gln Glu Ala Val Trp Glu Ala Tyr Arg Ile
            100                 105                 110

Phe Leu Asp Arg Ile Pro Asp Thr Gly Glu Tyr Gln Asp Trp Val Ser
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Ser Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile Lys Gln
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Arg Ser Phe Pro Asp Arg Lys Asp Glu Ile Ser Ala Glu Lys Thr Leu
            165             170             175

Gly Glu Pro Gly Glu Thr Ile Val Ile Ser Thr Asp Val Ala Asn Val
            180             185             190

Ser Leu Gly Pro Phe Pro Leu Thr Pro Asp Asp Thr Leu Leu Asn Glu
            195             200             205

Ile Leu Asp Asn Thr Leu Asn Asp Thr Lys Met Pro Thr Thr Glu Arg
    210             215             220

Glu Thr Glu Phe Ala Val Leu Glu Glu Gln Arg Val Glu Leu Ser Val
225             230             235             240

Ser Leu Val Asn Gln Lys Phe Lys Ala Glu Leu Ala Asp Ser Gln Ser
            245             250             255

Pro Tyr Tyr Gln Glu Leu Ala Gly Lys Ser Gln Leu Gln Met Gln Lys
            260             265             270

Ile Phe Lys Lys Leu Pro Gly Phe Lys Lys Ile His Val Leu Gly Phe
        275             280             285

Arg Pro Lys Lys Glu Lys Asp Gly Ser Ser Ser Thr Glu Met Gln Leu
    290             295             300

Thr Ala Ile Phe Lys Arg His Ser Ala Glu Ala Lys Ser Pro Ala Ser
305             310             315             320

Asp Leu Leu Ser Phe Asp Ser Asn Lys Ile Glu Ser Glu Glu Val Tyr
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His Gly Thr Met Glu Glu Asp Lys Gln Pro Glu Ile Tyr Leu Thr Ala
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Thr Asp Leu Lys Arg Leu Ile Ser Lys Ala Leu Glu Glu Glu Gln Ser
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Leu Asp Val Gly Thr Ile Gln Phe Thr Asp Glu Ile Ala Gly Ser Leu
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Pro Ala Phe Gly Pro Asp Thr Gln Ser Glu Leu Pro Thr Ser Phe Ala
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Val Ile Thr Glu Asp Ala Thr Leu Ser Pro Glu Leu Pro Pro Val Glu
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Ile Pro Thr Ser Asp Tyr Ser Ala Ile Ser Gln Leu Ala Leu Gly Ile
            485             490                 495

Ser His Pro Pro Ala Ser Ser Asp Asp Ser Arg Ser Ser Ala Gly Gly
        500             505             510

Glu Asp Met Val Arg His Leu Asp Glu Met Asp Leu Ser Asp Thr Pro
    515             520             525

Ala Pro Ser Glu Val Pro Glu Leu Ser Glu Tyr Val Ser Val Pro Asp
    530             535             540

His Phe Leu Glu Asp Thr Thr Pro Val Ser Ala Leu Gln Tyr Ile Thr
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Thr Ser Ser Met Thr Ile Ala Pro Lys Gly Arg Glu Leu Val Val Phe
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Phe Ser Leu Arg Val Ala Asn Met Ala Phe Ser Asn Asp Leu Phe Asn
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Lys Ser Ser Leu Glu Tyr Arg Ala Leu Glu Gln Gln Phe Thr Gln Leu
        595             600             605

Leu Val Pro Tyr Leu Arg Ser Asn Leu Thr Gly Phe Lys Gln Leu Glu
    610             615             620

Ile Leu Asn Phe Arg Asn Gly Ser Val Ile Val Asn Ser Lys Met Lys
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Phe Ala Lys Ser Val Pro Tyr Asn Leu Thr Lys Ala Val His Gly Val
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Leu Glu Asp Phe Arg Ser Ala Ala Ala Gln Gln Leu His Leu Glu Ile
        660             665             670

Asp Ser Tyr Ser Leu Asn Ile Glu Pro Ala Asp Gln Ala Asp Pro Cys
        675             680             685

Lys Phe Leu Ala Cys Gly Glu Phe Ala Gln Cys Val Lys Asn Glu Arg
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Thr Glu Glu Ala Glu Cys Arg Cys Lys Pro Gly Tyr Asp Ser Gln Gly
705             710             715                 720

Ser Leu Asp Gly Leu Glu Pro Gly Leu Cys Gly Pro Gly Thr Lys Glu
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Cys Glu Val Leu Gln Gly Lys Gly Ala Pro Cys Arg Leu Pro Asp His
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Ser Glu Asn Gln Ala Tyr Lys Thr Ser Val Lys Lys Phe Gln Asn Gln
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<213> Homo sapiens

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Arg Ile Phe Leu Asp Arg Ile Pro Asp Thr Gly Glu Tyr Gln Asp Trp
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Val Ser Ile Cys Gln Gln Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys
    50                  55                  60

Asn Phe Ser Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile
65                  70                  75                  80

Lys Gln Arg Ser Phe Pro Asp Arg Lys Asp Glu Ile Ser Ala Glu Lys
            85                  90                  95

Thr Leu Gly Glu Pro Gly Glu Thr Ile Val Ile Ser Thr Asp Val Ala
            100                 105                 110

Asn Val Ser Leu Gly Pro Phe Pro Leu Thr Pro Asp Asp Thr Leu Leu
            115                 120                 125

Asn Glu Ile Leu Asp Asn Thr Leu Asn Asp Thr Lys Met Pro Thr Thr
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Glu Arg Glu Thr Glu Phe Ala Val Leu Glu Glu Gln Arg Val Glu Leu
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Gln Ser Pro Tyr Tyr Gln Glu Leu Ala Gly Lys Ser Gln Leu Gln Met
            180                 185                 190

Gln Lys Ile Phe Lys Lys Leu Pro Gly Phe Lys Lys Ile His Val Leu
            195                 200                 205

Gly Phe Arg Pro Lys Lys Glu Lys Asp Gly Ser Ser Ser Thr Glu Met
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Gln Leu Thr Ala Ile Phe Lys Arg His Ser Ala Glu Ala Lys Ser Pro
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6

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Val Tyr His Gly Thr Met Glu Glu Asp Lys Gln Pro Glu Ile Tyr Leu
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Thr Ala Thr Asp Leu Lys Arg Leu Ile Ser Lys Ala Leu Glu Glu Glu
            275             280             285

Gln Ser Leu Asp Val Gly Thr Ile Gln Phe Thr Asp Glu Ile Ala Gly
    290             295             300

Ser Leu Pro Ala Phe Gly Pro Asp Thr Gln Ser Glu Leu Pro Thr Ser
305             310             315             320

Phe Ala Val Ile Thr Glu Asp Ala Thr Leu Ser Pro Glu Leu Pro Pro
            325             330             335

Val Glu Pro Gln Leu Glu Thr Val Asp Gly Ala Glu His Gly Leu Pro
            340             345             350

Asp Thr Ser Trp Ser Pro Pro Ala Met Ala Ser Thr Ser Leu Ser Glu
            355             360             365

Ala Pro Pro Phe Phe Met Ala Ser Ser Ile Phe Ser Leu Thr Asp Gln
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Gly Thr Thr Asp Thr Met Ala Thr Asp Gln Thr Met Leu Val Pro Gly
385             390             395             400

Leu Thr Ile Pro Thr Ser Asp Tyr Ser Ala Ile Ser Gln Leu Ala Leu
            405             410             415

Gly Ile Ser His Pro Pro Ala Ser Ser Asp Asp Ser Arg Ser Ser Ala
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Gly Gly Glu Asp Met Val Arg His Leu Asp Glu Met Asp Leu Ser Asp
            435             440             445

Thr Pro Ala Pro Ser Glu Val Pro Gly Leu Ser Glu Tyr Val Ser Val
    450             455             460

Pro Asp His Phe Leu Glu Asp Thr Thr Pro Val Ser Ala Leu Gln Tyr
465             470             475             480

Ile Thr Thr Ser Ser Met Thr Ile Ala Pro Lys Gly Arg Glu Leu Val
            485             490             495

Val Phe Phe Ser Leu Arg Val Ala Asn Met Ala Phe Ser Asn Asp Leu
            500             505             510

Phe Asn Lys Ser Ser Leu Glu Tyr Arg Ala Leu Glu Gln Gln Phe Thr
            515             520             525

Gln Leu Leu Val Pro Tyr Leu Arg Ser Asn Leu Thr Gly Phe Lys Gln
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Leu Glu Ile Leu Asn Phe Arg Asn Gly Ser Val Ile Val Asn Ser Lys
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Gly Val Leu Glu Asp Phe Arg Ser Ala Ala Ala Gln Gln Leu His Leu
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Glu Ile Asp Ser Tyr Ser Leu Asn Ile Glu Pro Ala Asp Gln Ala Asp
          595             600             605

Pro Cys Lys Phe Leu Ala Cys Gly Glu Phe Ala Gln Cys Val Lys Asn
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Glu Arg Thr Glu Glu Ala Glu Cys Arg Cys Lys Pro Gly Tyr Asp Ser
625             630             635             640

Gln Gly Ser Leu Asp Gly Leu Glu Pro Gly Leu Cys Gly Pro Gly Thr
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Lys Glu Cys Glu Val Leu Gln Gly Lys Gly Ala Pro Cys Arg Leu Pro
          660             665             670

Asp His Ser Glu Asn Gln Ala Tyr Lys Thr Ser Val Lys Lys Phe Gln
      675             680             685

Asn Gln Gln Asn Asn Lys Val Ile Ser Lys Arg Asn Ser Glu Leu Leu
      690             695             700

Thr Val Glu Tyr Glu Glu Phe Asn His Gln Asp Trp Glu Gly Asn
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ccgagagctg gtagtgttct tcagtctgcg tgttgctaac atggccttct ccaacgacct 1980
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cgggagtgtg attgtgaata gcaaaatgaa gtttgctaag tcagtgccgt ataacctcac 2160
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<210> 6
<211> 198
<212> PRT
<213> Homo sapiens

<220>
<223> Human IPM 150 amino acid sequence, isoform C

<400> 6
Met Tyr Leu Glu Thr Arg Arg Ala Ile Phe Val Phe Trp Ile Phe Leu
 1               5                  10                  15

Gln Val Gln Gly Thr Lys Asp Ile Ser Ile Asn Ile Tyr His Ser Glu
                20                  25                  30

Thr Lys Asp Ile Asp Asn Pro Pro Arg Asn Glu Thr Thr Glu Ser Thr
            35                  40                  45

Glu Lys Met Tyr Lys Met Ser Thr Met Arg Arg Ile Phe Asp Leu Ala
        50                  55                  60

Lys His Arg Thr Lys Arg Ser Ala Phe Phe Pro Thr Gly Val Lys Val
65                  70                  75                  80

Cys Pro Gln Glu Ser Met Lys Gln Ile Leu Asp Ser Leu Gln Ala Tyr
                85                  90                  95

Tyr Arg Leu Arg Val Cys Gln Glu Ala Ala Trp Glu Ala Tyr Arg Ile
            100                 105                 110

Phe Leu Asp Arg Ile Pro Asp Thr Gly Glu Tyr Gln Asp Trp Val Ser
        115                 120                 125

Ile Cys Gln Gln Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys Asn Phe
    130                 135                 140
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Ser Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile Lys Gln
145             150             155             160

Arg Ser Phe Pro Asp Arg Lys Asp Glu Ile Ser Ala Glu Lys Thr Leu
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Gly Glu Pro Gly Glu Thr Ile Val Ile Ser Thr Ala Ile Tyr Ile Ser
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Lys Thr Trp Ala Val Phe
        195
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<210> 7
<211> 1858
<212> DNA
<213> Homo sapiens

<220>
<223> Human IMPG1 gene, regulatory region

<220>
<221> misc_feature
<222> (1)..(1858)
<223> n is a, c, g, or t.

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aatctatgga taatctatgg acatctctaa gaacaatgtc tatccacaac acaagagctc 180
aatatacagt agtagttgca gtgtgtttca tgactcagca atatgtagca tgtatagtca 240
aaataatata aaatcaaata ttcaaaaact gaaattacaa taatactgat gaagaaagat 300
ggaaagatgt ttacaatgag tagaaagggt atgtgtggaa gtgaagttat tctcaatatc 360
tattatttga taatacctaa aagtgaaaac ctccaaaata gtaatagagg catgttattt 420
agaagtgcaa atgagactac tagaagaatt aggttgatga agtaaaaatg ctcccctttt 480
gaaagaaggc atgggtagaa gaaaggcaca atttttttctt acaaactttg tagaaaaaaa 540
gtatttgacc ccttaaacac agtgcataca gatttttaaac attaaaacca gacttaaatc 600
aaaaaagcca cctgtatgta attccaaatc aaaagcaatt tataaagcag aacatagaag 660
agaatggaga cagtttcgct atctgtggag actaatacat attggataac catatacttt 720
cagggacaga aattaagctc ttttaatgga tgtttcttgt acatgtcatt ttagaaaaca 780
tctgacccta actgtcagcc ttattctctg tttggcagaa cttcccctgg ctctctgtgt 840
cactgtaaca ggtgaataac taagaaaaaa ctgtgtctgt agacacttgt ttataatggc 900
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gaaacagaca ctgctacatg ttcttcataa attaacaccc tcataaaggt aaaccaagaa 1080
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gatttaatat ttactacatg gtcttaagtg cagtgaagat taacaaaata ggagagatga 1500
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<210> 8
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<211> 3668
<212> DNA
<213> Mus sp.

<220>
<223> Mouse IPM 150 cDNA sequence, isoform A

<220>
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<222> (1)..(3668)
<223> n is a, c, g, or t.

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cagtcacctt atttctttaa gtgtgacttg gtattgttct gtgatttttc agaattacca 180
gtatacagaa ccagaatgaa ttttcaaatt aaacatgcta tctttgtttt tgggattttt 240
ctccaagttc aaggaatcaa agatacctct attaaaatat tcagttctga aattaaaaac 300
atagacaaaa ccccaagaat cgaaacaatt gaaagtactt caacagtgca caaagtgtca 360
accatgaaac gaatattcga tttgccaaag cttcgaacca aaagatcagc acttttccca 420
gctgctaaca tctgtccaca ggaatccttg agacagattt tagcaagtct tcaagaatat 480
tatagactga gagtatgtca agaagtcgtg tgggaagcat atcgtatctt tctggaccga 540
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ctctttgaca ttgggaaaaa cttcagcaac tcccaggagc acctagatct tcttcagcag 660
agaataaaac agagaagctt ccctgggagg aaagatgaga cagcctccat ggagacactg 720
gaagcaccta ctgaagcccc tgtggtaccc acagatgttt ccaggatgtc cctggggccc 780
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attcaaaagc ccacaacaga aagtaaaaca gaacctattc acgtgtctga attctcatca 900
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gcagaagcaa aaagccctga tagtcatcta ctgtctcttg attccaacaa aattgaaagt 1200
gaaagaatcc atcatggagt catagaagac aaacaaccag aaacctacct cacagctaca 1260
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<210> 9
<211> 798
<212> PRT
<213> Mus sp.

<220>
<223> Mouse IPM 150 amino acid sequence, isoform A

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Met Asn Phe Gln Ile Lys His Ala Ile Phe Val Phe Gly Ile Phe Leu
1               5                   10                  15

Gln Val Gln Gly Ile Lys Asp Thr Ser Ile Lys Ile Phe Ser Ser Glu
                20                  25                  30

Ile Lys Asn Ile Asp Lys Thr Pro Arg Ile Glu Thr Ile Glu Ser Thr
        35                  40                  45

Ser Thr Val His Lys Val Ser Thr Met Lys Arg Ile Phe Asp Leu Pro
    50                  55                  60

Lys Leu Arg Thr Lys Arg Ser Ala Leu Phe Pro Ala Ala Asn Ile Cys
65              70                  75                  80

Pro Gln Glu Ser Leu Arg Gln Ile Leu Ala Ser Leu Gln Glu Tyr Tyr
                85                  90                  95

Arg Leu Arg Val Cys Gln Glu Val Val Trp Glu Ala Tyr Arg Ile Phe
            100                 105                 110

Leu Asp Arg Ile Pro Asp Thr Glu Glu Tyr Gln Asp Trp Val Ser Leu
        115                 120                 125

Cys Gln Lys Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys Asn Phe Ser
    130                 135                 140

Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile Lys Gln Arg
145                 150                 155                 160

Ser Phe Pro Gly Arg Lys Asp Glu Thr Ala Ser Met Glu Thr Leu Glu
                165                 170                 175

Ala Pro Thr Glu Ala Pro Val Val Pro Thr Asp Val Ser Arg Met Ser
            180                 185                 190
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Leu Gly Pro Phe Pro Leu Pro Ser Asp Asp Thr Asp Leu Lys Glu Ile
        195             200             205

Leu Ser Val Thr Leu Lys Asp Ile Gln Lys Pro Thr Thr Glu Ser Lys
        210             215             220

Thr Glu Pro Ile His Val Ser Glu Phe Ser Ser Glu Glu Lys Val Glu
225             230             235             240

Phe Ser Ile Ser Leu Pro Asn His Arg Phe Lys Ala Glu Leu Thr Asn
            245             250             255

Ser Gly Ser Pro Tyr Tyr Gln Glu Leu Val Gly Gln Ser Gln Leu Gln
            260             265             270

Leu Gln Lys Ile Phe Lys Lys Leu Pro Gly Phe Gly Glu Ile Arg Val
        275             280             285

Leu Gly Phe Arg Pro Lys Lys Glu Glu Asp Gly Ser Ser Ser Thr Glu
        290             295             300

Ile Gln Leu Met Ala Ile Phe Lys Arg Asp His Ala Glu Ala Lys Ser
305             310             315             320

Pro Asp Ser His Leu Leu Ser Leu Asp Ser Asn Lys Ile Glu Ser Glu
            325             330             335

Arg Ile His His Gly Val Ile Glu Asp Lys Gln Pro Glu Thr Tyr Leu
            340             345             350

Thr Ala Thr Asp Leu Lys Lys Leu Ile Ile Gln Leu Leu Asp Gly Asp
        355             360             365

Leu Ser Leu Val Glu Gly Lys Ile Pro Phe Gly Asp Glu Val Thr Gly
        370             375             380

Thr Leu Phe Arg Pro Val Thr Glu Pro Asp Leu Pro Lys Pro Leu Ala
385             390             395             400

Asp Val Thr Glu Asp Ala Thr Leu Ser Pro Glu Leu Pro Phe Val Glu
            405             410             415

Pro Arg Leu Glu Ala Val Asp Arg Glu Gly Ser Glu Leu Pro Gly Met
        420             425             430

Ser Ser Lys Asp Ser Ser Trp Ser Pro Pro Val Ser Ala Ser Ile Ser
        435             440             445

Arg Ser Glu Asn Leu Pro Ser Phe Thr Pro Ser Ile Phe Ser Leu Asp
        450             455             460

Ala Gln Ser Pro Pro Pro Leu Met Thr Thr Gly Pro Thr Ala Leu Ile
465             470             475             480

Pro Lys Pro Thr Leu Pro Thr Ile Asp Tyr Ser Thr Ile Arg Gln Leu
            485             490             495

Pro Leu Glu Ser Ser His Trp Pro Ala Ser Ser Ser Asp Arg Glu Leu
            500             505             510
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Ile Thr Ser Ser His Asp Thr Ile Arg Asp Leu Asp Gly Met Asp Val
        515             520             525

Ser Asp Thr Pro Ala Leu Ser Glu Ile Ser Glu Leu Ser Gly Tyr Asp
        530             535             540

Ser Ala Ser Gly Gln Phe Leu Glu Met Thr Thr Pro Ile Pro Thr Val
545             550             555             560

Arg Phe Ile Thr Thr Ser Ser Glu Thr Ile Ala Thr Lys Gly Gln Glu
                565             570             575

Leu Val Val Phe Phe Ser Leu Arg Val Ala Asn Met Pro Phe Ser Tyr
                580             585             590

Asp Leu Phe Asn Lys Ser Ser Leu Glu Tyr Gln Ala Leu Glu Gln Arg
        595             600             605

Phe Thr Asp Leu Leu Val Pro Tyr Leu Arg Ser Asn Leu Thr Gly Phe
        610             615             620

Lys Gln Leu Glu Ile Leu Ser Phe Arg Asn Gly Ser Val Ile Val Asn
625             630             635             640

Ser Lys Val Arg Phe Ala Lys Ala Val Pro Tyr Asn Leu Thr Gln Ala
                645             650             655

Val Arg Gly Val Leu Glu Asp Leu Arg Ser Thr Ala Ala Gln Gly Leu
                660             665             670

Asn Leu Glu Ile Glu Ser Tyr Ser Leu Asp Ile Glu Pro Ala Asp Gln
        675             680             685

Ala Asp Pro Cys Lys Leu Leu Asp Cys Gly Lys Phe Ala Gln Cys Val
        690             695             700

Lys Asn Glu Trp Thr Glu Glu Ala Glu Cys Arg Cys Arg Gln Gly His
705             710             715             720

Glu Ser His Gly Thr Leu Asp Tyr Gln Thr Leu Asn Leu Cys Pro Pro
                725             730             735

Gly Lys Thr Cys Val Ala Gly Arg Glu Gln Ala Thr Pro Cys Arg Pro
                740             745             750

Pro Asp His Ser Thr Asn Gln Ala Gln Glu Pro Gly Val Lys Lys Leu
        755             760             765

Arg Gln Gln Asn Lys Val Val Lys Lys Arg Asn Ser Lys Leu Ser Ala
        770             775             780

Ile Gly Phe Glu Glu Phe Glu Asp Gln Asp Trp Glu Gly Asn
785             790             795
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<210> 10
<211> 1726
<212> DNA
<213> Mus sp.

<220>

<223> Mouse IPM 150 cDNA sequence, isoform D

<400> 10
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accagtatac agaaccagaa tgaattttca aattaaacat gctatctttg tttttgggat 180
ttttctccaa gttcaaggaa tcaaagtatg tcaagaagtc gtgtgggaag catatcgtat 240
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tcttcttcag cagagaataa aacagagaag cttccctggg aggaaagatg agacagcctc 420
catggagaca ctggaagcac ctactgaagc ccctgtggta cccacagatg tttccaggat 480
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caccctcaag gacattcaaa agcccacaac agaaagtata acagaaccta ttcacgtgtc 600
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gcagttgcaa aagatattta agaaacttcc aggattcgga gaaatccgtg tattaggatt 780
tagaccaaag aaagaagaag atggttcaag ctccacagaa atacagctta tggccatctt 840
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<210> 11
<211> 466
<212> PRT
<213> Mus sp.

<220>
<223> Mouse IPM 150 amino acid sequence, isoform D

<400> 11
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Gln Val Gln Gly Ile Lys Val Cys Gln Glu Val Val Trp Glu Ala Tyr
            20                  25                  30


Arg Ile Phe Leu Asp Arg Ile Pro Asp Thr Glu Glu Tyr Gln Asp Trp
        35                  40                  45


Val Ser Leu Cys Gln Lys Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys
    50                  55                  60


Asn Phe Ser Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile
65                  70                  75                  80


Lys Gln Arg Ser Phe Pro Gly Arg Lys Asp Glu Thr Ala Ser Met Glu
                85                  90                  95
```

```
Thr Leu Glu Ala Pro Thr Glu Ala Pro Val Val Pro Thr Asp Val Ser
            100             105                 110

Arg Met Ser Leu Gly Pro Phe Pro Leu Pro Ser Asp Asp Thr Asp Leu
            115             120                 125

Lys Glu Ile Leu Ser Val Thr Leu Lys Asp Ile Gln Lys Pro Thr Thr
    130             135                 140

Glu Ser Ile Thr Glu Pro Ile His Val Ser Glu Phe Ser Ser Glu Glu
145             150                 155                 160

Lys Val Glu Phe Ser Ile Ser Leu Pro Asn His Arg Phe Lys Ala Glu
            165             170                 175

Leu Thr Asn Ser Gly Ser Pro Tyr Tyr Gln Glu Leu Val Gly Gln Ser
            180             185                 190

Gln Leu Gln Leu Gln Lys Ile Phe Lys Lys Leu Pro Gly Phe Gly Glu
            195             200                 205

Ile Arg Val Leu Gly Phe Arg Pro Lys Lys Glu Glu Asp Gly Ser Ser
    210             215                 220

Ser Thr Glu Ile Gln Leu Met Ala Ile Phe Lys Arg Asp His Ala Glu
225             230             235                 240

Ala Lys Ser Pro Asp Ser His Leu Leu Ser Leu Asp Ser Asn Lys Ile
            245             250                 255

Glu Ser Glu Arg Ile His His Gly Val Ile Glu Asp Lys Gln Pro Glu
            260             265                 270

Thr Tyr Leu Thr Ala Thr Asp Leu Lys Lys Leu Ile Ile Gln Leu Leu
            275             280                 285

Asp Gly Asp Leu Ser Leu Val Glu Gly Lys Ile Pro Phe Gly Asp Glu
    290             295                 300

Val Thr Gly Thr Leu Phe Arg Pro Val Thr Glu Pro Asp Leu Pro Lys
305             310             315                 320

Pro Leu Ala Asp Val Thr Glu Asp Ala Thr Leu Ser Pro Glu Leu Pro
            325             330                 335

Phe Val Glu Pro Arg Leu Glu Ala Val Asp Arg Glu Gly Ser Glu Leu
            340             345                 350

Pro Ala Asp Gln Ala Asp Pro Cys Lys Leu Leu Asp Cys Gly Lys Phe
            355             360                 365

Ala Gln Cys Val Lys Asn Glu Trp Thr Glu Glu Ala Glu Cys Arg Cys
    370             375                 380

Arg Gln Gly His Glu Ser His Gly Thr Leu Asp Tyr Gln Thr Leu Asn
385             390                 395                 400

Leu Cys Pro Pro Gly Lys Thr Cys Val Ala Gly Arg Glu Gln Ala Thr
            405             410                 415
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16

Pro Cys Arg Pro Thr Asp His Ser Thr Asn Gln Ala Gln Glu Pro Gly
            420   425   430

Val Lys Lys Leu Arg Gln Gln Asn Lys Val Val Lys Lys Arg Asn Ser
        435   440   445

Lys Leu Ser Ala Ile Gly Phe Glu Glu Phe Glu Asp Gln Asp Trp Glu
    450   455   460

Gly Asn
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<210> 12
<211> 1321
<212> DNA
<213> Mus sp.

<220>
<223> Mouse IPM 150 cDNA sequence, isoform E

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cgattctgcc tcgggtcagt tcttggagat gaccacaccc atcccaacag tacggttcat 420
caccaccagc tccgagacca ttgccaccaa gggccaggag ctagtggtat tcttcagcct 480
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cgggaccctg gactaccaga ccctgaacct ctgtccccct ggaaagactt gtgtggccgg 960
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ctgttctgtt aacttctgaa aaacagaggg agagattcag tggtcattgg aatacaggca 1260
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<210> 13
<211> 67
<212> PRT
<213> Mus sp.

<220>
<223> Mouse IPM 150 amino acid sequence, isoform E

<400> 13
Met Asn Phe Gln Ile Lys His Ala Ile Phe Val Phe Gly Ile Phe Leu
1   5   10   15

Gln Val Gln Gly Ile Lys Asp Thr Ser Ile Lys Ile Phe Ser Ser Glu
            20   25   30

Ile Lys Asn Ile Asp Lys Thr Pro Arg Ile Glu Thr Ile Glu Ser Thr
          35   40   45

Ser Thr Val His Lys Val Ser Thr Met Lys Arg Gln Pro Cys Gln Lys
     50   55   60

Tyr Gln Asn
 65

<210> 14
<211> 555
<212> DNA
<213> Unknown Organism

<220>
<223> Monkey IPM 150 cDNA (partial)

<220>
<223> Description of Unknown Organism: Monkey species

<400> 14
attttctttc cgaacggggt taaagtctgt ccacaggaat ccatgaaaca gattttagcc 60
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atctttctgg atcgcatccc tgacacaggg gaatatcagg actgggtcag cttctgccag 180
caggagacct tctgcctctt tgacatcgga caaaacttca gcaattccca ggagcacctg 240
gatcttctcc agcagagaat aaaacagaga agtttccctg agagaaaaga tgaagtatct 300
acagagaaga cattgggaga gcctagtgaa accattgtgg tttcaacaga tgttgccagc 360
gtctcacttg ggcctttccc tgtcactcct gatgacaccc tcctcaatga aattctcgat 420
aatgcactca acgacaccaa gatgcctaca acagaaagag aaacagaact cgctgtgtct 480
gaggagcaga gggtggagct cagcatctct ctgataaacc agaggttcaa ggcagagctc 540
gctgactctc agtca   555

<210> 15
<211> 185
<212> PRT
<213> Unknown Organism

<220>
<223> Description of Unknown Organism: Monkey species

<220>
<223> Monkey IPM 150 amino acid sequence (partial).

<400> 15
Ile Phe Phe Pro Asn Gly Val Lys Val Cys Pro Gln Glu Ser Met Lys
 1   5   10   15

Gln Ile Leu Ala Ser Leu Gln Ala Tyr Tyr Arg Leu Arg Val Cys Gln
             20   25   30

Glu Ala Val Trp Glu Ala Tyr Arg Ile Phe Leu Asp Arg Ile Pro Asp
         35   40   45

Thr Gly Glu Tyr Gln Asp Trp Val Ser Phe Cys Gln Gln Glu Thr Phe
     50   55   60

Cys Leu Phe Asp Ile Gly Gln Asn Phe Ser Asn Ser Gln Glu His Leu
 65   70   75   80

18

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Asp Leu Leu Gln Gln Arg Ile Lys Gln Arg Ser Phe Pro Glu Arg Lys
                 85                  90                  95

Asp Glu Val Ser Thr Glu Lys Thr Leu Gly Glu Pro Ser Glu Thr Ile
             100             105             110

Val Val Ser Thr Asp Val Ala Ser Val Ser Leu Gly Pro Phe Pro Val
         115             120             125

Thr Pro Asp Asp Thr Leu Leu Asn Glu Ile Leu Asp Asn Ala Leu Asn
     130             135             140

Asp Thr Lys Met Pro Thr Thr Glu Arg Glu Thr Glu Leu Ala Val Ser
145             150             155             160

Glu Glu Gln Arg Val Glu Leu Ser Ile Ser Leu Ile Asn Gln Arg Phe
             165             170             175

Lys Ala Glu Leu Ala Asp Ser Gln Ser
             180             185


<210> 16
<211> 4166
<212> DNA
<213> Homo sapiens

<220>
<223> Human IPM 200 (isoform A) cDNA

<400> 16
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tggaagtttc aaggatttgg acactcaatt aaggattctg cctctcctc attcctttgg 180
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ctctagctac caaaaagaaa cagcctctgg accgcagaga aactgaaaga cagtggttaa 420
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aatctgtgga acatagaagc ttaatcatga agaaactgac ttatgcaaag gaaactgtaa 720
gcagctctga actgtcttct ccagttcctg ttggtgatac ttcaacattg ggagacacta 780
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<210> 17
<211> 1241
<212> PRT
<213> Homo sapiens

<220>
<223> Human IPM 200 amino acid sequence, isoform A

<400> 17
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Met Ile Met Phe Pro Leu Phe Gly Lys Ile Ser Leu Gly Ile Leu Ile
 1               5                  10                  15


Phe Val Leu Ile Glu Gly Asp Phe Pro Ser Leu Thr Ala Gln Thr Tyr
            20                  25                  30


Leu Ser Ile Glu Glu Ile Gln Glu Pro Lys Ser Ala Val Ser Phe Leu
        35                  40                  45
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Leu Pro Glu Glu Ser Thr Asp Leu Ser Leu Ala Thr Lys Lys Lys Gln
    50              55              60

Pro Leu Asp Arg Arg Glu Thr Glu Arg Gln Trp Leu Ile Arg Arg Arg
65              70              75              80

Arg Ser Ile Leu Phe Pro Asn Gly Val Lys Ile Cys Pro Asp Glu Ser
                85              90              95

Val Ala Glu Ala Val Ala Asn His Val Lys Tyr Phe Lys Val Arg Val
            100             105             110

Cys Gln Glu Ala Val Trp Glu Ala Phe Arg Thr Phe Trp Asp Arg Leu
        115             120             125

Pro Gly Arg Glu Glu Tyr His Tyr Trp Met Asn Leu Cys Glu Asp Gly
    130             135             140

Val Thr Ser Ile Phe Glu Met Gly Thr Asn Phe Ser Glu Ser Val Glu
145             150             155             160

His Arg Ser Leu Ile Met Lys Lys Leu Thr Tyr Ala Lys Glu Thr Val
            165             170             175

Ser Ser Ser Glu Leu Ser Ser Pro Val Pro Val Gly Asp Thr Ser Thr
            180             185             190

Leu Gly Asp Thr Thr Leu Ser Val Pro His Pro Glu Val Asp Ala Tyr
        195             200             205

Glu Gly Ala Ser Glu Ser Ser Leu Glu Arg Pro Glu Glu Ser Ile Ser
    210             215             220

Asn Glu Ile Glu Asn Val Ile Glu Glu Ala Thr Lys Pro Ala Gly Glu
225             230             235             240

Gln Ile Ala Glu Phe Ser Ile His Leu Leu Gly Lys Gln Tyr Arg Glu
                245             250             255

Glu Leu Gln Asp Ser Ser Ser Phe His His Gln His Leu Glu Glu Glu
        260             265             270

Phe Ile Ser Glu Val Glu Asn Ala Phe Thr Gly Leu Pro Gly Tyr Lys
        275             280             285

Glu Ile Arg Val Leu Glu Phe Arg Ser Pro Lys Glu Asn Asp Ser Gly
    290             295             300

Val Asp Val Tyr Tyr Ala Val Thr Phe Asn Gly Glu Ala Ile Ser Asn
305             310             315             320

Thr Thr Trp Asp Leu Ile Ser Leu His Ser Asn Lys Val Glu Asn His
            325             330             335

Gly Leu Val Glu Leu Asp Asp Lys Pro Thr Val Val Tyr Thr Ile Ser
        340             345             350

Asn Phe Arg Asp Tyr Ile Ala Glu Thr Leu Gln Gln Asn Phe Leu Leu
    355             360             365
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Gly Asn Ser Ser Leu Asn Pro Asp Pro Asp Ser Leu Gln Leu Ile Asn
    370                 375             380

Val Arg Gly Val Leu Arg His Gln Thr Glu Asp Leu Val Trp Asn Thr
385                 390             395                 400

Gln Ser Ser Ser Leu Gln Ala Thr Pro Ser Ser Ile Leu Asp Asn Thr
                405             410                 415

Phe Gln Ala Ala Trp Pro Ser Ala Asp Glu Ser Ile Thr Ser Ser Ile
            420             425             430

Pro Pro Leu Asp Phe Ser Ser Gly Pro Pro Ser Ala Thr Gly Arg Glu
        435             440             445

Leu Trp Ser Glu Ser Pro Leu Gly Asp Leu Val Ser Thr His Lys Leu
    450             455             460

Ala Phe Pro Ser Lys Met Gly Leu Ser Ser Ser Pro Glu Val Leu Glu
465             470             475                 480

Val Ser Ser Leu Thr Leu His Ser Val Thr Pro Ala Val Leu Gln Thr
            485             490             495

Gly Leu Pro Val Ala Ser Glu Glu Arg Thr Ser Gly Ser His Leu Val
        500             505             510

Glu Asp Gly Leu Ala Asn Val Glu Glu Ser Glu Asp Phe Leu Ser Ile
        515             520             525

Asp Ser Leu Pro Ser Ser Ser Phe Thr Gln Pro Val Pro Lys Glu Thr
    530             535             540

Ile Pro Ser Met Glu, Asp Ser Asp Val Ser Leu Thr Ser Ser Pro Tyr
545             550             555                 560

Leu Thr Ser Ser Ile Pro Phe Gly Leu Asp Ser Leu Thr Ser Lys Val
            565             570             575

Lys Asp Gln Leu Lys Val Ser Pro Phe Leu Pro Asp Ala Ser Met Glu
        580             585             590

Lys Glu Leu Ile Phe Asp Gly Gly Leu Gly Ser Gly Ser Gly Gln Lys
        595             600             605

Val Asp Leu Ile Thr Trp Pro Trp Ser Glu Thr Ser Ser Glu Lys Ser
    610             615             620

Ala Glu Pro Leu Ser Lys Pro Trp Leu Glu Asp Asp Ser Leu Leu
625             630             635                 640

Pro Ala Glu Ile Glu Asp Lys Lys Leu Val Leu Val Asp Lys Met Asp
            645             650             655

Ser Thr Asp Gln Ile Ser Lys His Ser Lys Tyr Glu His Asp Asp Arg
        660             665             670

Ser Thr His Phe Pro Glu Glu Glu Pro Leu Ser Gly Pro Ala Val Pro
        675             680             685
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Ile Phe Ala Asp Thr Ala Ala Glu Ser Ala Ser Leu Thr Leu Pro Lys
    690                 695             700

His Ile Ser Glu Val Pro Gly Val Asp Asp Cys Ser Val Thr Lys Ala
705                 710             715                 720

Pro Leu Ile Leu Thr Ser Val Ala Ile Ser Ala Ser Thr Asp Lys Ser
                725             730             735

Asp Gln Ala Asp Ala Ile Leu Arg Glu Asp Met Glu Gln Ile Thr Glu
            740             745             750

Ser Ser Asn Tyr Glu Trp Phe Asp Ser Glu Val Ser Met Val Lys Pro
        755             760             765

Asp Met Gln Thr Leu Trp Thr Ile Leu Pro Glu Ser Glu Arg Val Trp
    770             775             780

Thr Arg Thr Ser Ser Leu Glu Lys Leu Ser Arg Asp Ile Leu Ala Ser
785             790             795             800

Thr Pro Gln Ser Ala Asp Arg Leu Trp Leu Ser Val Thr Gln Ser Thr
            805             810             815

Lys Leu Pro Pro Thr Thr Ile Ser Thr Leu Leu Glu Asp Glu Val Ile
            820             825             830

Met Gly Val Gln Asp Ile Ser Leu Glu Leu Asp Arg Ile Gly Thr Asp
        835             840             845

Tyr Tyr Gln Pro Glu Gln Val Gln Glu Gln Asn Gly Lys Val Gly Ser
    850             855             860

Tyr Val Glu Met Ser Thr Ser Val His Ser Thr Glu Met Val Ser Val
865             870             875             880

Ala Trp Pro Thr Glu Gly Gly Asp Asp Leu Ser Tyr Thr Gln Thr Ser
            885             890             895

Gly Ala Leu Val Val Phe Phe Ser Leu Arg Val Thr Asn Met Met Phe
        900             905             910

Ser Glu Asp Leu Phe Asn Lys Asn Ser Leu Glu Tyr Lys Ala Leu Glu
    915             920             925

Gln Arg Phe Leu Glu Leu Leu Val Pro Tyr Leu Gln Ser Asn Leu Thr
    930             935             940

Gly Phe Gln Asn Leu Glu Ile Leu Asn Phe Arg Asn Gly Ser Ile Val
945             950             955             960

Val Asn Ser Arg Met Lys Phe Ala Asn Ser Val Pro Pro Asn Val Asn
            965             970             975

Asn Ala Val Tyr Met Ile Leu Glu Asp Phe Cys Thr Thr Ala Tyr Asn
        980             985             990

Thr Met Asn Leu Ala Ile Asp Lys Tyr Ser Leu Asp Val Glu Ser Gly
        995             1000            1005
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Asp Glu Ala Asn Pro Cys Lys Phe Gln Ala Cys Asn Glu Phe Ser Glu
  1010   1015   1020

Cys Leu Val Asn Pro Trp Ser Gly Glu Ala Lys Cys Arg Cys Phe Pro
1025   1030   1035   1040

Gly Tyr Leu Ser Val Glu Glu Arg Pro Cys Gln Ser Leu Cys Asp Leu
        1045   1050   1055

Gln Pro Asp Phe Cys Leu Asn Asp Gly Lys Cys Asp Ile Met Pro Gly
      1060   1065   1070

His Gly Ala Ile Cys Arg Cys Arg Val Gly Glu Asn Trp Trp Tyr Arg
      1075   1080   1085

Gly Lys His Cys Glu Glu Phe Val Ser Glu Pro Val Ile Ile Gly Ile
  1090   1095   1100

Thr Ile Ala Ser Val Val Gly Leu Leu Val Ile Phe Ser Ala Ile Ile
1105   1110   1115   1120

Tyr Phe Phe Ile Arg Thr Leu Gln Ala His His Asp Arg Ser Glu Arg
        1125   1130   1135

Glu Ser Pro Phe Ser Gly Ser Ser Arg Gln Pro Asp Ser Leu Ser Ser
        1140   1145   1150

Ile Glu Asn Ala Val Lys Tyr Asn Pro Val Tyr Glu Ser His Arg Ala
      1155   1160   1165

Gly Cys Glu Lys Tyr Glu Gly Pro Tyr Pro Gln His Pro Phe Tyr Ser
  1170   1175   1180

Ser Ala Ser Gly Asp Val Ile Gly Gly Leu Ser Arg Glu Glu Ile Arg
1185   1190   1195   1200

Gln Met Tyr Glu Ser Ser Glu Leu Ser Arg Glu Glu Ile Gln Glu Arg
        1205   1210   1215

Met Arg Val Leu Glu Leu Tyr Ala Asn Asp Pro Glu Phe Ala Ala Phe
      1220   1225   1230

Val Arg Glu Gln Gln Val Glu Glu Val
      1235   1240

<210> 18
<211> 2964
<212> DNA
<213> Homo sapiens

<220>
<223> Human IPM 200 cDNA sequence, isoform C

<400> 18
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attcttagaa ttgctggttc cctatctcca gtcaaatctc acggggttcc agaacttaga 2700
aatcctcaac ttcagaaatg gcagcattgt ggtgaacagt cgaatgaagt ttgccaattc 2760
tgtccctcct aacgtcaaca atgcggtgta catgattctg gaagactttt gtaccactgc 2820
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<210> 19
<211> 432
<212> PRT
<213> Homo sapiens

<220>
<223> Human IPM 200 amino acid sequence, isoform C

<220>
<221> UNSURE
<222> (1)..(432)
<223> Xaa is any amino acid.

<400> 19

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Phe Val Leu Ile Glu Gly Asp Phe Pro Ser Leu Thr Ala Gln Thr Tyr
                20              25                  30

Leu Ser Ile Glu Glu Ile Gln Glu Pro Lys Ser Ala Val Ser Phe Leu
            35                  40                  45

Leu Pro Glu Glu Ser Thr Asp Leu Ser Leu Ala Thr Lys Lys Lys Gln
    50                  55                  60

Pro Leu Asp Arg Arg Glu Thr Glu Arg Gln Trp Leu Ile Arg Arg Arg
65                  70                  75                  80

Arg Ser Ile Leu Phe Pro Asn Gly Val Lys Ile Cys Pro Asp Glu Ser
                85                  90                  95

Val Ala Glu Ala Val Ala Asn His Val Lys Tyr Phe Lys Val Arg Val
            100                 105                 110

Cys Gln Glu Ala Val Trp Glu Ala Phe Arg Thr Phe Trp Asp Xaa Leu
        115                 120                 125

Pro Gly Arg Glu Glu Tyr His Tyr Trp Met Asn Leu Cys Glu Asp Gly
    130                 135                 140

Val Thr Ser Ile Phe Glu Met Gly Thr Asn Phe Ser Glu Ser Val Glu
145                 150                 155                 160

His Arg Ser Leu Ile Met Lys Lys Leu Thr Tyr Ala Lys Glu Thr Val
                165                 170                 175

Ser Ser Ser Glu Leu Ser Ser Pro Val Pro Val Gly Asp Thr Ser Thr
            180                 185                 190

Leu Gly Asp Thr Thr Leu Ser Val Pro His Pro Glu Val Asp Ala Tyr
        195                 200                 205

Glu Gly Ala Ser Glu Ser Ser Leu Glu Arg Pro Glu Glu Ser Ile Ser
    210                 215                 220

Asn Glu Ile Glu Asn Val Ile Glu Glu Ala Thr Lys Pro Ala Gly Glu
225                 230                 235                 240

Gln Ile Ala Glu Phe Ser Ile His Leu Leu Gly Lys Gln Tyr Arg Glu
                245                 250                 255

Glu Leu Gln Asp Ser Ser Ser Phe His His Gln His Leu Glu Glu Glu
        260                 265                 270

Phe Ile Ser Glu Val Glu Asn Ala Phe Thr Gly Leu Pro Gly Tyr Lys
    275                 280                 285

Glu Ile Arg Val Leu Glu Phe Arg Ser Pro Lys Glu Asn Asp Ser Gly
    290                 295                 300

Val Asp Val Tyr Tyr Ala Val Thr Phe Asn Gly Glu Ala Ile Ser Asn
305                 310                 315                 320
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Thr Thr Trp Asp Leu Ile Ser Leu His Ser Asn Lys Val Glu Asn His
            325   330   335

Gly Leu Val Glu Leu Asp Asp Lys Pro Thr Val Val Tyr Thr Ile Ser
            340   345   350

Asn Phe Arg Asp Tyr Ile Ala Glu Thr Leu Gln Gln Asn Phe Leu Leu
            355   360   365

Gly Asn Ser Ser Leu Asn Pro Asp Pro Asp Ser Leu Gln Leu Ile Asn
            370   375   380

Val Arg Gly Val Leu Arg His Gln Thr Glu Asp Leu Val Trp Asn Thr
385   390   395   400

Gln Ser Ser Ser Leu Gln Ala Thr Pro Ser Ser Ile Leu Cys Phe Xaa
            405   410   415

Leu Ala Cys Leu Trp Leu Leu Arg Lys Gly Leu Leu Asp Leu Thr Trp
            420   425   430

<210> 20
<211> 861
<212> DNA
<213> Homo sapiens

<220>
<223> Human IPM 200 cDNA sequence, isoform F

<400> 20
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ttgtcctgat agaaggagac tttccatcat taacagcaca aacctactta tctatagagg 180
agatccaagc actgtgagga atttgtgtct gagcccgtga tcataggcat cactattgcc 240
tccgtggttg gacttcttgt catcttttct gctatcatct acttcttcat caggactctt 300
caagcacacc atgacaggag tgaaagagag agtcccttca gtggctccag caggcagcct 360
gacagcctct catctattga gaatgctgtg aagtacaacc cgtgtatga aagtcacagg 420
gctggatgtg agaagtatga gggaccctat cctcagcatc ccttctacag ctctgctagc 480
ggagacgtga ttggtgggct gagcagagaa gaaatcagac agatgtatga gagcagtgag 540
ctttccagag aggaaattca agagagaatg agagttttgg aactgtatgc caatgatcct 600
gagtttgcag cttttgtgag agagcaacaa gtggaagagg tttaaccaaa actcctgttc 660
tgaaactgat tagaagcctg agaagatgg agattacttg ttacttatgt catataatta 720
acctggattt taaacactgt tggaagaaga gttttctatg aaaaaattaa atataggggca 780
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<210> 21
<211> 41
<212> PRT
<213> Homo sapiens

<220>
<223> Human IPM 200 amino acid sequence, isoform F

<400> 21

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Met Ile Met Phe Pro Leu Phe Gly Lys Ile Ser Leu Gly Ile Leu Ile
  1                 5                 10                15

Phe Val Leu Ile Glu Gly Asp Phe Pro Ser Leu Thr Ala Gln Thr Tyr
                20                25                30

Leu Ser Ile Glu Glu Ile Gln Ala Leu
        35                40


<210> 22
<211> 3011
<212> DNA
<213> Homo sapiens

<220>
<223> Human IPM 200, regulatory region

<220>
<221> misc_feature
<222> (1)..(3011)
<223> n ia a, c, g, or t.

<400> 22
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gattatcaca tgtaatttct ttggtgagta aaccggctca aagagcttag gttatttacc 180
aaaatcaaat attaagtgat aaaaccaaga tttgagtcca gggtttctca atcttaaata 240
caggaatctt tctagattac tatgattctc agaagttttt tttagctttt tggtcaaggc 300
tgtcaaaaag aataattgcc aacttaatat ttgttaccta agagttgtcc cttgttctga 360
attgtcaata tgaagctttt cttaagatta aactttgact cagctaataa aattttcggc 420
ttttttctcc tactcataca ataaatttgg caagtaagtt cttataagc ttaccagtat 480
tttgcaaata caactatgca aatatattta atggtcattt aggtttatta gctttttataa 540
aggctgaaaa tgtggtttat ttgaggctgt attgaaaaaa tatacttgag ctttttcctaa 600
agcataaaat aacattgagg gtgatttagc taacacaatt agtcaaggat tctcaagagg 660
aatgtggttt agatctttac aatacacttt ttttcagaga attttgccag agataacatg 720
aaataaaata taatttcatt gctatttgat agtaaatcca agcttccaca gggattctga 780
tgaattgctt tctactaggt ttacttgatt taaaaaactg ttctaatata gagaatttca 840
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cacatttaat ggcaaattaa gcaacaaagt tatcgcacag ctatcattta tattaagtgc 960
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<210> 23
<211> 4204
<212> DNA
<213> Mus sp.

<220>
<223> Mouse IPM 200 cDNA sequence (partial)

<220>
<221> misc_feature
<222> (1)..(4204)
<223> n is a, c, g, or t.

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tatgtgagga tggagtcaca agtgtatttg aaatgggcgc ccattttagt cagtctgtgg 180
aacatagaaa cctaatcatg aagaaactgg cttacacaag ggaagctgag agcagctcct 240
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ggaa                                                                 4204
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<210> 24
<211> 1069
<212> PRT
<213> Mus sp.

<220>
<223> Mouse IPM 200 amino acid sequence (partial)

<220>
<221> UNSURE
<222> (1)..(1069)
<223> Xaa is any amino acid.

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Ile Trp Glu Ala Phe Arg Thr Phe Trp Asp Arg Leu Pro Gly Arg Asp
            20   25   30

30

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Glu Tyr Arg His Trp Met Asn Leu Cys Glu Asp Gly Val Thr Ser Val
        35                  40                  45

Phe Glu Met Gly Ala His Phe Ser Gln Ser Val Glu His Arg Asn Leu
        50                  55                  60

Ile Met Lys Lys Leu Ala Tyr Thr Arg Glu Ala Glu Ser Ser Ser Cys
65                  70                  75                  80

Lys Asp Gln Ser Cys Gly Pro Glu Leu Ser Phe Pro Val Pro Ile Gly
                85                  90                  95

Glu Thr Ser Thr Leu Thr Gly Ala Val Ser Ser Ala Ser Tyr Pro Gly
            100                 105                 110

Leu Ala Ser Glu Ser Ser Ala Ala Ser Pro Gln Glu Ser Ile Ser Asn
            115                 120                 125

Glu Ile Glu Asn Val Thr Glu Glu Pro Thr Gln Pro Ala Ala Glu Gln
    130                 135                 140

Ile Ala Glu Phe Ser Ile Gln Leu Leu Gly Lys Arg Tyr Ser Glu Glu
145                 150                 155                 160

Leu Arg Asp Pro Ser Ser Ala Leu Tyr Arg Leu Leu Val Glu Glu Phe
                165                 170                 175

Ile Ser Glu Val Glu Lys Ala Phe Thr Gly Leu Pro Gly Tyr Lys Gly
            180                 185                 190

Ile Arg Val Leu Glu Phe Arg Ala Pro Glu Glu Asn Asp Ser Gly Ile
            195                 200                 205

Asp Val His Tyr Ala Val Thr Phe Asn Gly Glu Ala Ile Ser Asn Thr
    210                 215                 220

Thr Trp Asp Leu Ile Ser Leu His Ser Asn Lys Val Glu Asn His Gly
225                 230                 235                 240

Leu Val Glu Met Asp Asp Lys Pro Thr Ala Val Tyr Thr Ile Ser Asn
                245                 250                 255

Phe Arg Asp Tyr Ile Ala Glu Thr Leu His Gln Asn Phe Leu Met Gly
            260                 265                 270

Asn Ser Ser Leu Asn Pro Asp Pro Lys Pro Leu Gln Leu Ile Asn Val
            275                 280                 285

Arg Gly Val Leu Leu Pro Gln Thr Glu Asp Ile Val Trp Asn Thr Gln
    290                 295                 300

Ser Ser Ser Leu Gln Val Thr Thr Ser Ser Ile Xaa Val Leu Gln Pro
305                 310                 315                 320

Asp Leu Pro Val Ala Pro Glu Gly Arg Thr Ser Gly Ser Phe Ile Leu
            325                 330                 335

Glu Asp Gly Leu Ala Ser Thr Glu Glu Leu Glu Asp Thr Ser Ile Asp
            340                 345                 350
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Gly Leu Pro Ser Ser Pro Leu Ile Gln Pro Val Pro Lys Glu Thr Val
        355   360   365

Pro Pro Met Glu Asp Ser Asp Thr Ala Leu Leu Ser Thr Pro His Leu
        370   375   380

Thr Ser Ser Ala Ile Glu Asp Leu Thr Lys Asp Ile Gly Thr Pro Ser
385   390   395   400

Gly Leu Glu Ser Leu Ala Ser Asn Ile Ser Asp Gln Leu Glu Val Ile
                405   410   415

Pro Trp Phe Pro Asp Thr Ser Val Glu Lys Asp Phe Ile Phe Glu Ser
            420   425   430

Gly Leu Gly Ser Gly Ser Gly Lys Asp Val Asp Val Ile Asp Trp Pro
        435   440   445

Trp Ser Glu Thr Ser Leu Glu Lys Thr Thr Lys Pro Leu Ser Lys Ser
    450   455   460

Trp Ser Glu Glu Gln Asp Ala Leu Leu Pro Thr Glu Gly Arg Glu Lys
465   470   475   480

Leu His Ile Asp Gly Arg Val Asp Ser Thr Glu Gln Ile Ile Glu Ser
            485   490   495

Ser Glu His Arg Tyr Gly Asp Arg Pro Ile His Phe Ile Glu Glu Xaa
        500   505   510

Ser His Val Arg Ser Thr Ile Pro Ile Phe Val Glu Ser Ala Thr Pro
        515   520   525

Pro Thr Ser Pro Ile Phe Ser Lys His Thr Ser Asp Val Pro Asp Ile
        530   535   540

Asp Ser Tyr Ser Leu Thr Lys Pro Pro Phe Leu Pro Val Thr Ile Ala
545   550   555   560

Ile Pro Ala Ser Thr Lys Lys Thr Asp Glu Val Leu Lys Glu Asp Met
                565   570   575

Val His Thr Glu Ser Ser Ser His Lys Glu Leu Asp Ser Glu Val Pro
            580   585   590

Val Ser Arg Pro Asp Met Gln Pro Val Trp Thr Met Leu Pro Glu Ser
        595   600   605

Asp Thr Val Trp Thr Arg Thr Ser Ser Leu Gly Lys Leu Ser Arg Asp
    610   615   620

Thr Leu Ala Ser Thr Pro Glu Ser Thr Asp Arg Leu Trp Leu Lys Ala
625   630   635   640

Ser Met Thr Gln Ser Thr Glu Leu Pro Ser Thr Thr His Ser Thr Gln
                645   650   655

Leu Glu Glu Glu Val Ile Met Ala Val Gln Asp Ile Ser Leu Glu Leu
            660   665   670

Asp Gln Val Gly Thr Asp Tyr Tyr Gln Ser Glu Leu Thr Glu Glu Gln
        675   680   685

His Gly Lys Ala Asp Ser Tyr Val Glu Met Ser Thr Ser Val His Tyr
        690   695   700

Thr Glu Met Pro Ile Val Ala Leu Pro Thr Lys Gly Gly Val Leu Ser
705   710   715   720

His Thr Gln Thr Ala Gly Ala Leu Val Val Phe Phe Ser Leu Arg Val
            725   730   735

Thr Asn Met Leu Phe Ser Glu Asp Leu Phe Asn Lys Asn Ser Leu Glu
        740   745   750

Tyr Lys Ala Leu Glu Gln Arg Phe Leu Glu Leu Leu Ala Pro Tyr Leu
        755   760   765

Gln Ser Asn Leu Ser Gly Phe Gln Asn Leu Glu Ile Leu Ser Phe Arg
        770   775   780

Asn Gly Ser Ile Val Val Asn Ser Arg Val Arg Phe Ala Glu Ser Ala
785   790   795   800

Pro Pro Asn Val Asn Lys Ala Met Tyr Arg Ile Leu Glu Asp Phe Cys
                805   810   815

Thr Thr Ala Tyr Gln Thr Met Asn Leu Asp Ile Asp Lys Tyr Ser Leu
            820   825   830

Asp Val Glu Ser Gly Asp Glu Ala Asn Pro Cys Lys Phe Gln Ala Cys
        835   840   845

Asn Glu Phe Ser Glu Cys Leu Val Asn Pro Trp Ser Gly Glu Ala Lys
        850   855   860

Cys Lys Cys Tyr Pro Gly Tyr Leu Ser Val Asp Glu Leu Pro Cys Gln
865   870   875   880

Ser Leu Cys Asp Leu Gln Pro Asp Phe Cys Leu Asn Asp Gly Lys Cys
            885   890   895

Asp Ile Met Pro Gly His Gly Ala Ile Cys Arg Cys Arg Val Gly Ser
            900   905   910

Asn Trp Trp Tyr Arg Gly Gln His Cys Glu Glu Phe Val Ser Glu Pro
        915   920   925

Phe Val Ile Gly Ile Thr Ile Ala Ser Val Val Ser Phe Leu Leu Val
        930   935   940

Ala Ser Ala Val Val Phe Phe Leu Val Lys Met Leu Gln Ala Gln Asn
945   950   955   960

Val Arg Arg Glu Arg Gln Arg Pro Thr Ser Ser Ser Arg His Pro Asp
            965   970   975

Ser Leu Ser Ser Val Glu Asn Ala Met Lys Tyr Asn Pro Ala Tyr Glu
            980   985   990

```
Ser His Leu Ala Gly Cys Glu Leu Tyr Glu Lys Ser Tyr Ser Gln His
     995               1000               1005

Pro Phe Tyr Ser Ser Ala Ser Glu Glu Val Ile Gly Gly Leu Ser Arg
    1010               1015               1020

Glu Glu Ile Arg Gln Met Tyr Glu Ser Ser Asp Leu Ser Lys Glu Glu
1025               1030               1035               1040

Ile Gln Glu Arg Met Arg Ile Leu Glu Leu Tyr Ala Asn Asp Pro Glu
              1045               1050               1055

Phe Ala Ala Phe Val Arg Glu His Gln Met Glu Glu Leu
         1060               1065
```

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<210> 25
<211> 546
<212> DNA
<213> Macaca fascicularis

<220>
<223> Monkey IPM 200 cDNA sequence (partial)

<400> 25
gaattcggct tggacaacca tttttctttc cgctaattta taatggtttt gaagtggttg 60
ttcattctca aacatagact tttaaatgtt aggtctttcc tataacttgt tgttattgga 120
agtttcaagg atttggacgc tcagttaagg attttgtcct ctcctcattc ctttggtttt 180
ggcccaaatg attatgtttc ctcttttggg aagatttct ctgggtattt tgatatttgt 240
cctgatagga gactttccat cgttaacagc acaaacctac ttatctttag aggagatcca 300
agaacccaag agtgcagttt cttttctcct gcctgaagaa tcaacagacc tttctctagc 360
taccaaaaag aaacagcctc tggacctcag agaaactgaa agacagtggt tactcagaag 420
gcggagatct attctgtttc ctaatggagt aaaaatctgc ccagatgaaa gtgttacaga 480
ggctgtggca aatcatgtga agtattttaa agtccgagtg tgtcaggaag ctgtctggga 540
aaagcc                                                           546
```

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<210> 26
<211> 119
<212> PRT
<213> Macaca fascicularis

<220>
<223> Monkey IPM 200 amino acid sequence (partial)

<400> 26
Met Ile Met Phe Pro Leu Phe Gly Lys Ile Ser Leu Gly Ile Leu Ile
  1               5                  10                  15

Phe Val Leu Ile Gly Asp Phe Pro Ser Leu Thr Ala Gln Thr Tyr Leu
              20                  25                  30

Ser Leu Glu Glu Ile Gln Glu Pro Lys Ser Ala Val Ser Phe Leu Leu
         35                  40                  45

Pro Glu Glu Ser Thr Asp Leu Ser Leu Ala Thr Lys Lys Lys Gln Pro
    50                  55                  60

Leu Asp Leu Arg Glu Thr Glu Arg Gln Trp Leu Leu Arg Arg Arg Arg
 65                  70                  75                  80
```

```
Ser Ile Leu Phe Pro Asn Gly Val Lys Ile Cys Pro Asp Glu Ser Val
                85                  90                  95

Thr Glu Ala Val Ala Asn His Val Lys Tyr Phe Lys Val Arg Val Cys
            100                 105                 110

Gln Glu Ala Val Trp Glu Lys
        115


<210> 27
<211> 3261
<212> DNA
<213> Homo sapiens

<220>
<223> Human IPM 150 isoform A variant cDNA sequence

<220>
<221> CDS
<222> (128)..(2440)

<400> 27
taaaccaaga aggttatcct caatcatctg gtatcaatat ataattattt ttcctttntg 60

ttactttta atgagatttg aggttgttct gtgattgtta tcagaattac catgcacaaa 120

agccaga atg tat ttg gaa act aga aga gct att ttt gtt ttt tgg att      169
        Met Tyr Leu Glu Thr Arg Arg Ala Ile Phe Val Phe Trp Ile
          1               5                  10

ttt ctc caa gtt caa gga act aaa gat atc tcc att aac ata tac cat      217
Phe Leu Gln Val Gln Gly Thr Lys Asp Ile Ser Ile Asn Ile Tyr His
 15                  20                  25                  30

tct gaa act aaa gac ata gac aat ccc cca aga aat gaa aca act gaa      265
Ser Glu Thr Lys Asp Ile Asp Asn Pro Pro Arg Asn Glu Thr Thr Glu
                35                  40                  45

agt act gaa aaa atg tac aaa atg tca act atg aga cga ata ttc gat.     313
Ser Thr Glu Lys Met Tyr Lys Met Ser Thr Met Arg Arg Ile Phe Asp
            50                  55                  60

ttg gca aag cat cga aca aaa aga tcc gca ttt ttc cca acg ggg gtt      361
Leu Ala Lys His Arg Thr Lys Arg Ser Ala Phe Phe Pro Thr Gly Val
            65                  70                  75

aaa gtc tgt cca cag gaa tcc atg aaa cag att tta gac agt ctt caa      409
Lys Val Cys Pro Gln Glu Ser Met Lys Gln Ile Leu Asp Ser Leu Gln
        80                  85                  90

gct tat tat aga ttg aga gtg tgt cag gaa gca gta tgg gaa gca tat      457
Ala Tyr Tyr Arg Leu Arg Val Cys Gln Glu Ala Val Trp Glu Ala Tyr
 95                 100                 105                 110

cgg atc ttt ctg gat cgc atc cct gac aca ggg gaa tat cag gac tgg      505
Arg Ile Phe Leu Asp Arg Ile Pro Asp Thr Gly Glu Tyr Gln Asp Trp
            115                 120                 125
```

```
gtc agc atc tgc cag cag gag acc ttc tgc ctc ttt gac att gga aaa    553
Val Ser Ile Cys Gln Gln Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys
            130                 135                 140

aac ttc agc aat tcc cag gag cac ctg gat ctt ctc cag cag aga ata    601
Asn Phe Ser Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile
            145                 150                 155

aaa cag aga agt ttc cct gac aga aaa gat gaa ata tct gca gag aag    649
Lys Gln Arg Ser Phe Pro Asp Arg Lys Asp Glu Ile Ser Ala Glu Lys
            160                 165                 170

aca ttg gga gag cct ggt gaa acc att gtc att tca aca gat gtt gcc    697
Thr Leu Gly Glu Pro Gly Glu Thr Ile Val Ile Ser Thr Asp Val Ala
175                 180                 185                 190

aac gtc tca ctt ggg cct ttc cct ctc act cct gat gac acc ctc ctc    745
Asn Val Ser Leu Gly Pro Phe Pro Leu Thr Pro Asp Asp Thr Leu Leu
                195                 200                 205

aat gaa att ctc gat aat aca ctc aac gac acc aag atg cct aca aca    793
Asn Glu Ile Leu Asp Asn Thr Leu Asn Asp Thr Lys Met Pro Thr Thr
            210                 215                 220

gaa aga gaa aca gaa ttc gct gtg ttg gag gag cag agg gtg gag ctc    841
Glu Arg Glu Thr Glu Phe Ala Val Leu Glu Glu Gln Arg Val Glu Leu
            225                 230                 235

agc gtc tct ctg gta aac cag aag ttc aag gca gag ctc gct gac tcc    889
Ser Val Ser Leu Val Asn Gln Lys Phe Lys Ala Glu Leu Ala Asp Ser
    240                 245                 250

cag tcc cca tat tac cag gag cta gca gga aag tcc caa ctt cag atg    937
Gln Ser Pro Tyr Tyr Gln Glu Leu Ala Gly Lys Ser Gln Leu Gln Met
255                 260                 265                 270

caa aag ata ttt aag aaa ctt cca gga ttc aaa aaa atc cat gtg tta    985
Gln Lys Ile Phe Lys Lys Leu Pro Gly Phe Lys Lys Ile His Val Leu
                275                 280                 285

gga ttt aga cca aag aaa gaa aaa gat ggc tca agc tcc aca gag atg   1033
Gly Phe Arg Pro Lys Lys Glu Lys Asp Gly Ser Ser Ser Thr Glu Met
                290                 295                 300

caa ctt acg gcc atc ttt aag aga cac agt gca gaa gca aaa agc cct   1081
Gln Leu Thr Ala Ile Phe Lys Arg His Ser Ala Glu Ala Lys Ser Pro
            305                 310                 315

gca agt gac ctc ctg tct ttt gat tcc aac aaa att gaa agt gag gaa   1129
Ala Ser Asp Leu Leu Ser Phe Asp Ser Asn Lys Ile Glu Ser Glu Glu
            320                 325                 330

gtc tat cat gga acc atg gag gag gac aag caa cca gaa atc tat ctc   1177
Val Tyr His Gly Thr Met Glu Glu Asp Lys Gln Pro Glu Ile Tyr Leu
335                 340                 345                 350

aca gct aca gac ctc aaa agg ctg atc agc aaa gca cta gag gaa gaa   1225
Thr Ala Thr Asp Leu Lys Arg Leu Ile Ser Lys Ala Leu Glu Glu Glu
            355                 360                 365
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caa tct ttg gat gtg ggg aca att cag ttc act gat gaa att gct gga      1273
Gln Ser Leu Asp Val Gly Thr Ile Gln Phe Thr Asp Glu Ile Ala Gly
            370                 375                 380

tca ctg cca gcc ttt ggt cct gac acc caa tca gag ctg ccc aca tct      1321
Ser Leu Pro Ala Phe Gly Pro Asp Thr Gln Ser Glu Leu Pro Thr Ser
            385                 390                 395

ttt gct gtt ata aca gag gat gct act ttg agt cca gaa ctt cct cct      1369
Phe Ala Val Ile Thr Glu Asp Ala Thr Leu Ser Pro Glu Leu Pro Pro
        400                 405                 410

gtt gaa ccc cag ctt gag aca gtg gac gga gca gag cat ggt cta cct      1417
Val Glu Pro Gln Leu Glu Thr Val Asp Gly Ala Glu His Gly Leu Pro
415                 420                 425                 430

gac act tct tgg tct cca cct gct atg gcc tct acc tcc ctg tca gaa      1465
Asp Thr Ser Trp Ser Pro Pro Ala Met Ala Ser Thr Ser Leu Ser Glu
                435                 440                 445

gct cca cct ttc ttt atg gca tca agc atc ttc tct ctg act gat caa      1513
Ala Pro Pro Phe Phe Met Ala Ser Ser Ile Phe Ser Leu Thr Asp Gln
            450                 455                 460

ggc acc aca gat aca atg gcc act gac cag aca atg cta gta cca ggg      1561
Gly Thr Thr Asp Thr Met Ala Thr Asp Gln Thr Met Leu Val Pro Gly
            465                 470                 475

ctc acc atc ccc acc agt gat tat tct gca atc agc caa ctg gct ctg      1609
Leu Thr Ile Pro Thr Ser Asp Tyr Ser Ala Ile Ser Gln Leu Ala Leu
        480                 485                 490

gga att tca cat cca cct gca tct tca gat gac agc cga tca agt gca      1657
Gly Ile Ser His Pro Pro Ala Ser Ser Asp Asp Ser Arg Ser Ser Ala
495                 500                 505                 510

ggt ggc gaa gat atg gtc aga cac cta gat gaa atg gat ctg tct gac      1705
Gly Gly Glu Asp Met Val Arg His Leu Asp Glu Met Asp Leu Ser Asp
                515                 520                 525

act cct gcc cca tct gag gta cca gag ctc agc gaa tat gtt tct gtc      1753
Thr Pro Ala Pro Ser Glu Val Pro Glu Leu Ser Glu Tyr Val Ser Val
                530                 535                 540

cca gat cat ttc ttg gag gat acc act cct gtc tca gct tta cag tat      1801
Pro Asp His Phe Leu Glu Asp Thr Thr Pro Val Ser Ala Leu Gln Tyr
            545                 550                 555

atc acc act agt tct atg acc att gcc ccc aag ggc cga gag ctg gta      1849
Ile Thr Thr Ser Ser Met Thr Ile Ala Pro Lys Gly Arg Glu Leu Val
            560                 565                 570

gtg ttc ttc agt ctg cgt gtt gct aac atg gcc ttc tcc aac gac ctg      1897
Val Phe Phe Ser Leu Arg Val Ala Asn Met Ala Phe Ser Asn Asp Leu
575                 580                 585                 590

ttc aac aag agc tct ctg gag tac cga gct ctg gag caa caa ttc aca      1945
Phe Asn Lys Ser Ser Leu Glu Tyr Arg Ala Leu Glu Gln Gln Phe Thr
            595                 600                 605
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cag ctg ctg gtt cca tat cta cga tcc aat ctt aca gga ttt aag caa   1993
Gln Leu Leu Val Pro Tyr Leu Arg Ser Asn Leu Thr Gly Phe Lys Gln
            610                 615             620

ctt gaa ata ctt aac ttc aga aac ggg agt gtg att gtg aat agc aaa   2041
Leu Glu Ile Leu Asn Phe Arg Asn Gly Ser Val Ile Val Asn Ser Lys
            625                 630             635

atg aag ttt gct aag tct gtg ccg tat aac ctc acc aag gct gtg cac   2089
Met Lys Phe Ala Lys Ser Val Pro Tyr Asn Leu Thr Lys Ala Val His
            640                 645             650

ggg gtc ttg gag gat ttt cgt tct gct gca gcc caa caa ctc cat ctg   2137
Gly Val Leu Glu Asp Phe Arg Ser Ala Ala Ala Gln Gln Leu His Leu
655                 660                 665                 670

gaa ata gac agc tac tct ctc aac att gaa cca gct gat caa gca gat   2185
Glu Ile Asp Ser Tyr Ser Leu Asn Ile Glu Pro Ala Asp Gln Ala Asp
                675                 680             685

ccc tgc aag ttc ctg gcc tgc ggc gaa ttt gcc caa tgt gta aag aac   2233
Pro Cys Lys Phe Leu Ala Cys Gly Glu Phe Ala Gln Cys Val Lys Asn
                690                 695             700

gaa cgg act gag gaa gcg gag tgt cgc tgc aaa cca gga tat gac agc   2281
Glu Arg Thr Glu Glu Ala Glu Cys Arg Cys Lys Pro Gly Tyr Asp Ser
            705                 710             715

cag ggg agc ctg gac ggt ctg gaa cca ggc ctc tgt ggc ctg gca caa   2329
Gln Gly Ser Leu Asp Gly Leu Glu Pro Gly Leu Cys Gly Leu Ala Gln
    720                 725                 730

agg aat gcg agg tcc tcc agg gaa agg gag ctc cat gcg gtt cca gat   2377
Arg Asn Ala Arg Ser Ser Arg Glu Arg Glu Leu His Ala Val Pro Asp
735                 740                 745                 750

cac tct gaa aat caa gca tac aaa act agt gtt aaa agt tcc aaa atc   2425
His Ser Glu Asn Gln Ala Tyr Lys Thr Ser Val Lys Ser Ser Lys Ile
                755                 760             765

aac aaa ata aca agg taatcagtaa aagaaattct gaattactga ccgtagaata   2480
Asn Lys Ile Thr Arg
                770

tgaagaattt aaccatcaag attgggaagg aaattaaaaa ctgaaaatgt acaattatca 2540

cttaggctat ctcaagagag atgatttgcc ttctcaagga aaatggagac aggcatattc 2600

atgggtcatc aaaatccaga catacagtca acactgagaa tcagcacaca ccatatttca 2660

aatatagaag agtcatgtac ttggcaacca gtaaattctg aaaaaaaaga cacttactta 2720

ttattaaaac cccaaatgca atcagcgaaa catattttta ctattcttgg atgatagtca 2780

aaatgatcat aagccaggtt tgcttccacc ttccctgaaa attttactca cagatcattt 2840

gcaacaagca tagcttactt attgtttagg gactgaacaa tttattggga agcaaactct 2900

ttatatgcta gaaagtacat ttaaaagatg actacttacg cagggagatg caggtctctc 2960

taaacgcatg aatgtatgta gtgtgtaggc actgtagtga gtgtatatat gctccacact 3020
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acgtctgata aacacaaacc tcagtattca gttattaggc acactagttt tatacgcaac 3080

tactgcttac atagtagact gttttgttgc caataatctt tgaattgttc tttaaaagaa 3140

actgaggttc agatacacat accatggaaa aatcttactt ttcttgttac tacacaaagc 3200

tattttaaag aagatgctat gttgggagaa gggcgaagtt gtactatatg acataatcaa 3260

t                                                             3261


<210> 28
<211> 771
<212> PRT
<213> Homo sapiens
<223> Human IPM 150 isoform A variant cDNA sequence

<400> 28
Met Tyr Leu Glu Thr Arg Arg Ala Ile Phe Val Phe Trp Ile Phe Leu
 1               5                  10                  15

Gln Val Gln Gly Thr Lys Asp Ile Ser Ile Asn Ile Tyr His Ser Glu
                20                  25                  30

Thr Lys Asp Ile Asp Asn Pro Pro Arg Asn Glu Thr Thr Glu Ser Thr
            35                  40                  45

Glu Lys Met Tyr Lys Met Ser Thr Met Arg Arg Ile Phe Asp Leu Ala
        50                  55                  60

Lys His Arg Thr Lys Arg Ser Ala Phe Phe Pro Thr Gly Val Lys Val
65                  70                  75                  80

Cys Pro Gln Glu Ser Met Lys Gln Ile Leu Asp Ser Leu Gln Ala Tyr
                85                  90                  95

Tyr Arg Leu Arg Val Cys Gln Glu Ala Val Trp Glu Ala Tyr Arg Ile
                100                 105                 110

Phe Leu Asp Arg Ile Pro Asp Thr Gly Glu Tyr Gln Asp Trp Val Ser
            115                 120                 125

Ile Cys Gln Gln Glu Thr Phe Cys Leu Phe Asp Ile Gly Lys Asn Phe
            130                 135                 140

Ser Asn Ser Gln Glu His Leu Asp Leu Leu Gln Gln Arg Ile Lys Gln
145                 150                 155                 160

Arg Ser Phe Pro Asp Arg Lys Asp Glu Ile Ser Ala Glu Lys Thr Leu
                165                 170                 175

Gly Glu Pro Gly Glu Thr Ile Val Ile Ser Thr Asp Val Ala Asn Val
                180                 185                 190

Ser Leu Gly Pro Phe Pro Leu Thr Pro Asp Asp Thr Leu Leu Asn Glu
            195                 200                 205

Ile Leu Asp Asn Thr Leu Asn Asp Thr Lys Met Pro Thr Thr Glu Arg
    210                 215                 220
```

Glu Thr Glu Phe Ala Val Leu Glu Glu Gln Arg Val Glu Leu Ser Val
225   230   235   240

Ser Leu Val Asn Gln Lys Phe Lys Ala Glu Leu Ala Asp Ser Gln Ser
                245   250   255

Pro Tyr Tyr Gln Glu Leu Ala Gly Lys Ser Gln Leu Gln Met Gln Lys
            260   265   270

Ile Phe Lys Lys Leu Pro Gly Phe Lys Lys Ile His Val Leu Gly Phe
        275   280   285

Arg Pro Lys Lys Glu Lys Asp Gly Ser Ser Ser Thr Glu Met Gln Leu
    290   295   300

Thr Ala Ile Phe Lys Arg His Ser Ala Glu Ala Lys Ser Pro Ala Ser
305   310   315   320

Asp Leu Leu Ser Phe Asp Ser Asn Lys Ile Glu Ser Glu Glu Val Tyr
            325   330   335

His Gly Thr Met Glu Glu Asp Lys Gln Pro Glu Ile Tyr Leu Thr Ala
            340   345   350

Thr Asp Leu Lys Arg Leu Ile Ser Lys Ala Leu Glu Glu Glu Gln Ser
        355   360   365

Leu Asp Val Gly Thr Ile Gln Phe Thr Asp Glu Ile Ala Gly Ser Leu
    370   375   380

Pro Ala Phe Gly Pro Asp Thr Gln Ser Glu Leu Pro Thr Ser Phe Ala
385   390   395   400

Val Ile Thr Glu Asp Ala Thr Leu Ser Pro Glu Leu Pro Pro Val Glu
            405   410   415

Pro Gln Leu Glu Thr Val Asp Gly Ala Glu His Gly Leu Pro Asp Thr
            420   425   430

Ser Trp Ser Pro Pro Ala Met Ala Ser Thr Ser Leu Ser Glu Ala Pro
        435   440   445

Pro Phe Phe Met Ala Ser Ser Ile Phe Ser Leu Thr Asp Gln Gly Thr
    450   455   460

Thr Asp Thr Met Ala Thr Asp Gln Thr Met Leu Val Pro Gly Leu Thr
465   470   475   480

Ile Pro Thr Ser Asp Tyr Ser Ala Ile Ser Gln Leu Ala Leu Gly Ile
            485   490   495

Ser His Pro Pro Ala Ser Ser Asp Asp Ser Arg Ser Ser Ala Gly Gly
            500   505   510

Glu Asp Met Val Arg His Leu Asp Glu Met Asp Leu Ser Asp Thr Pro
        515   520   525

Ala Pro Ser Glu Val Pro Glu Leu Ser Glu Tyr Val Ser Val Pro Asp
    530   535   540

```
His Phe Leu Glu Asp Thr Thr Pro Val Ser Ala Leu Gln Tyr Ile Thr
545             550             555                 560

Thr Ser Ser Met Thr Ile Ala Pro Lys Gly Arg Glu Leu Val Val Phe
                565             570                 575

Phe Ser Leu Arg Val Ala Asn Met Ala Phe Ser Asn Asp Leu Phe Asn
            580             585             590

Lys Ser Ser Leu Glu Tyr Arg Ala Leu Glu Gln Gln Phe Thr Gln Leu
            595             600             605

Leu Val Pro Tyr Leu Arg Ser Asn Leu Thr Gly Phe Lys Gln Leu Glu
    610             615             620

Ile Leu Asn Phe Arg Asn Gly Ser Val Ile Val Asn Ser Lys Met Lys
625             630             635             640

Phe Ala Lys Ser Val Pro Tyr Asn Leu Thr Lys Ala Val His Gly Val
            645             650             655

Leu Glu Asp Phe Arg Ser Ala Ala Ala Gln Gln Leu His Leu Glu Ile
            660             665             670

Asp Ser Tyr Ser Leu Asn Ile Glu Pro Ala Asp Gln Ala Asp Pro Cys
        675             680             685

Lys Phe Leu Ala Cys Gly Glu Phe Ala Gln Cys Val Lys Asn Glu Arg
    690             695             700

Thr Glu Glu Ala Glu Cys Arg Cys Lys Pro Gly Tyr Asp Ser Gln Gly
705             710             715                 720

Ser Leu Asp Gly Leu Glu Pro Gly Leu Cys Gly Leu Ala Gln Arg Asn
            725             730             735

Ala Arg Ser Ser Arg Glu Arg Glu Leu His Ala Val Pro Asp His Ser
            740             745             750

Glu Asn Gln Ala Tyr Lys Thr Ser Val Lys Ser Ser Lys Ile Asn Lys
    755             760             765

Ile Thr Arg
    770


<210> 29
<211> 20
<212> PRT
<213> Rattus sp.

<220>
<223> Rat IPM 200 N-terminal amino acid sequence

<400> 29
Ser Ile Leu Phe Pro Asn Gly Val Arg Ile Cys Pro Ser Asp Thr Val
 1               5                   10                  15

Ala Glu Ala Val
            20
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<210> 30
<211> 10
<212> PRT
<213> Pig species

<220>
<221> UNSURE
<222> (1)..(10)
<223> Xaa is any  amino acid.

<400> 30
Xaa Val Leu Phe Pro Asn Gly Val Lys Ile
 1               5                  10


<210> 31
<211> 20
<212> PRT
<213> Pig species

<220>
<221> MOD_RES
<222> (1)..(20)
<223> Xaa is any amino acid

<400> 31
Xaa Val Phe Phe Pro Thr Gly Val Lys Val Xaa Pro Gln Glu Ser Met
 1               5                  10                  15

Lys Gln Ile Leu
            20


<210> 32
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: RGD-containing
      peptide

<400> 32
Gly Arg Gly Asp Ser Pro
 1               5


<210> 33
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      RGD-containing peptide

<400> 33
Gly Arg Gly Asp Thr Pro
 1               5
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<210> 34
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<221> MOD_RES
<222> (2)
<223> Xaa is d-Arginine

<400> 34
Gly Xaa Gly Asp Ser Pro
  1               5


<210> 35
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: RGD-containing
      peptide

<220>
<221> MOD_RES
<222> (1)
<223> MeGly

<400> 35
Gly Arg Gly Asp Ser Pro
  1               5


<210> 36
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: RGD-containing
      peptide

<400> 36
Gly Arg Gly Asp Ser Pro Ala Ser Ser Lys
  1               5                   10


<210> 37
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Inhibitor

<220>
<221> MOD_RES
<222> (2)
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<223> Xaa is pencillamine

<400> 37
Gly Xaa Gly Arg Gly Asp Ser Pro Cys Ala
 1   5   10